

# Whole-Genome Sequences of Four *Salmonella enterica* Serotype Newport Strains from Humans

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**Salmonellosis contributes significantly to the public health burden globally. *Salmonella enterica* serotype Newport is among *Salmonella* serotypes most associated with food-borne illness in the United States and China. It was thought to be polyphyletic and to contain different lineages. We report draft genomes of four *S. Newport* strains isolated from humans in China.**

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Nontyphoidal *Salmonella* causes an estimated 93.8 million cases of gastroenteritis and 155,000 deaths each year in the world (1). *Salmonella enterica* serotype Newport ranks among the top three serotypes associated with food-borne illness in the United States, causing at least 100,000 infections annually (2). In China, *S. Newport* is also among the most common serotypes isolated from patients with diarrhea (3). The serotype was thought to be polyphyletic, with extensive genomic diversity, containing three independent lineages (4, 5).

Currently, a total of 32 completed genomes and 277 draft genomes of *Salmonella* have been deposited in GenBank, among which there were one completed genome and 27 draft genomes of *S. Newport*. Two of the genomes were from *S. Newport* strains isolated from clinical sources. In the present report, we announce the availability of four draft genomes of *S. Newport* strains from stool specimens of patients with diarrhea in China: SH111077, Shandong\_3, Henan\_3, and JS09102. The genome data provide insights on the genomic diversity and evolutionary history of *S. Newport*.

The four *S. Newport* strains were sequenced using the HiSeq 2000 platform (Illumina, San Diego, CA) to obtain 39 to 43× coverage draft genomes. Genomic data were assembled with SOAPdenovo 1.05 (<http://soap.genomics.org.cn/soapdenovo.html>). The data of each draft genome are as follows: SH111077 (80 contigs longer than 500 bp, genome size of 4,868,771 bp, and contig N<sub>50</sub> of 131,989), Shandong\_3 (55 contigs longer than 500 bp, genome size of 4,752,037 bp, and contig N<sub>50</sub> of 194,658), Henan\_3 (68 contigs longer than 500 bp, genome size of 4,812,853 bp, and contig N<sub>50</sub> of 183,174), and JS09102 (80 contigs longer than 500 bp, genome size of 5,078,742 bp, and contig N<sub>50</sub>

size of 160,516). Sequences were annotated with the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (6).

**Nucleotide sequence accession numbers.** The accession numbers of the four *S. Newport* genome sequences in GenBank are AOGJ000000000, AOGI000000000, AOGH000000000, and AOGG000000000.

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